CLAIM OR CLAIMS

WE CLAIM:

1. A microarray comprising a plurality of features, each of the features formed of single stranded oligonucleotides, at least some of the features including in the same feature oligonucleotides of more than one sequence.

2. A microarray as claimed in claim 1 wherein each feature includes oligonucleotides of two different sequences.

3. A microarray as claimed in claim 1 wherein at least some of the oligonucleotides in the microarray are oriented both 3' to 5' and at least some other oligonucleotides are oriented 5' to 3'.

4. A microarray as claimed in claim 1 wherein the two oligonucleotides in a single feature are each designed to hybridize to different exons in the same eukaryotic gene.

5. A microarray as claimed in claim 1 wherein the two probes each make up about 50% of the probes in the feature.

6. A method for synthesizing different oligonucleotides in the same feature area, the method comprising the steps of:

providing a substrate for manufacturing a microarray, the substrate having photo-labile protecting groups formed on its surface, the microarray having at least one feature area;

exposing the feature area to a light source for a period of time sufficient to cleave the photo-labile protecting group from only a portion of feature area;

coupling a second protecting group to the unprotected area of the feature, the second protective group not being photo-labile;

exposing the feature area to a light source for a period of time to cleave the remaining photo-labile protecting groups from the feature area to leave an unprotected area of the feature;

building a first group of oligonucleotides in the unprotected area of the feature;

capping the first group of oligonucleotides with a capping compound that is not photo-labile;

removing the second protecting group from the feature area to leave an unprotected area of the feature;

building a second group of oligonucleotides in the unprotected area of the feature.

7. The method of Claim 6 wherein the portion of the feature area in which the first light exposing step is conducted is about 50% of the feature area, so that each of the oligonucleotides is about 50% of the oligonucleotides in the feature.

8. The method of Claim 6 wherein the portion of the feature area in which the first light exposing step is conducted is about 33% of the feature area, so that one of the oligonucleotides is about 33% of the oligonucleotides in the feature..

9. The method of Claim 6 wherein the second protecting group is acid labile.

10. The method of Claim 9 wherein the second protective group is di-methoxy-trityl

11. The method of Claim 9 wherein the capping compound is acetic anhydride and tetrahydrofuran.

12. A method of using a microarray to analyze the splicing of an mRNA transcript from a gene having more than one exon, the method incorporating the steps of

providing a microarray with at least one feature two oligonucleotides in the feature, a first oligonucleotide being complementary to the mRNA in a portion of the mRNA corresponding to one exon and a second oligonucleotide corresponding in sequence to the mRNA in a portion corresponding to another exon;

hybridizing the microarray to the mRNA so that mRNA if present will bind to the nucleotide complementary to the mRNA;

extending the first oligonucleotide using the bound mRNA as a template;

removing the bound mRNA;

hybridizing the extended first oligonucleotide to the second oligonucleotide; and

extending the second oligonucleotide against first oligonucleotide using labeled nucleotides so that the feature can be detected if the hybridizations occurred.